

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Caras, Ingrid W

(ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 1 DNA Way

(C) CITY: South San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/635130

(B) FILING DATE: 19-Mar-1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Torchia, PhD., Timothy E.

(B) REGISTRATION NUMBER: 36,700

(C) REFERENCE/DOCKET NUMBER: P1001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-8674

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1877 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: Extra Cellular Domain

(B) LOCATION: 244-899

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Transmembrane Domain
- (B) LOCATION: 901-978
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: signal peptide
- (B) LOCATION: 244-321
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GNTCTAGAAN TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCCT 50
GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
TTTGGGGGAG TTGGTGCCCC GCCCCCCAGG CCTTGCGGGG GTC ATG 246
Met
1
GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
5 10
GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
15 20 25
CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
30 35 40
AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402
Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
45 50
ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
55 60 65
CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480
Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr
70 75

AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519
 Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys
 80 85 90

GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558
 Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
 95 100 105

CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597
 Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln
 110 115

GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636
 Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser
 120 125 130

CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675
 His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr
 135 140

CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714
 Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu
 145 150 155

ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753
 Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser
 160 165 170

CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792
 Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu
 175 180

ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831
 Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu
 185 190 195

GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870
 Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser
 200 205

AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT 909
 Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro
 210 215 220

CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG 948
 Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu
 225 230 235

GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987
 Ala Leu Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala

240

245

ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT 1026
Met Cys Trp Arg Arg Arg Arg Ala Lys Pro Ser Glu Ser
250 255 260

CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT 1065
Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser
265 270

CTG GGC CTG GGG GGT GGA GGT GGG ATG GGA CCT CGG GAG 1104
Leu Gly Leu Gly Gly Gly Gly Gly Met Gly Pro Arg Glu
275 280 285

GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC 1143
Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly
290 295 300

GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG 1182
Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys
305 310

GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG 1221
Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln
315 320 325

GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA 1260
Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr
330 335

TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA 1299
Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile
340 345 350

CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT 1338
Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr
355 360 365

ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377
Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr
370 375

TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416
Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro
380 385 390

TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455
Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg
395 400

				65					70					75	
Tyr	Glu	Phe	Tyr	Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	
				80					85					90	
Arg	Cys	Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	
				95					100					105	
Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	
				110					115					120	
Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	
				125					130					135	
Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	
				140					145					150	
Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	
				155					160					165	
Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	
				170					175					180	
Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	
				185					190					195	
Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	
				200					205					210	
Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	
				215					220					225	
Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	
				230					235					240	
Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	
				245					250					255	
Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	
				260					265					270	
Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	
				275					280					285	
Arg	Glu	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
				290					295					300	
Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	
				305					310					315	

Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	Asp	Gly	Pro	Pro	320	325	330
Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Thr	Ser	Ile	Ser	Val	Leu	Glu	335	340	345
Trp	Pro	Ile	Leu	His	Thr	Ile	Gln	Leu	Phe	Phe	Met	Arg	Ser	Lys	350	355	360
Cys	Ser	Arg	Val	Thr	Thr	Phe	Leu	Phe	Pro	Val	Gln	Val	Ile	Thr	365	370	375
Thr	Ser	Thr	Cys	Arg	Met	Thr	Ser	Phe	Ser	Phe	Thr	Thr	Leu	Asn	380	385	390
Pro	Ser	Met	Gln	Ala	Cys	Arg	Ala	Gln	Met	Gly	Glu	Phe	Arg	Ile	395	400	405
Arg	Trp	Cys	Phe	Trp	Gly	Asp	Arg	Ile	Leu	Gly	Thr	Ala	Leu	Phe	410	415	420
Val	Leu	Val	Leu	Ile	Leu	Leu	Leu	Gly	Arg	Leu	Asn	Met	His	Gln	425	430	435
Thr	Thr	Leu	Leu	Arg	Gln	Arg	Ala	Ser	Val	Glu	Ala	Glu	Ala	Gly	440	445	450
Gln	His	Gly	Pro	Leu											455		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GNTCTAGAAAN TAGTGGATCC CCCCAGGCTG CAGGAATTCC GACGGCCCCT 50
 GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
 CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
 CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
 TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGCGGGG GTCATGGGGC 250

CCCCCATTC TGGGCCGGGG GCGGTGCGAG TCGGGGCCCT GCTGCTGCTG 300
 GGGGTTTTGG GGCTGGTGTG TGGGCTCAGC CTGGAGCCTG TCTACTGGAA 350
 CTCGGCGAAT AAGAGGTTCC AGGCAGAGGG TGGTTATGTG CTGTACCCTC 400
 AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGCCCC GCCTCCTGGC 450
 CCTCACTCCT CTCCTAATTA TGAGTTCTAC AAGCTGTACC TGGTAGGGGG 500
 TGCTCAGGGC CGGCGCTGTG AGGCACCCCC TGCCCCAAAC CTCCTTCTCA 550
 CTTGTGATCG CCCAGACCTG GATCTCCGCT TCACCATCAA GTTCCAGGAG 600
 TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA 650
 CATCATTGCC ACATCGGATG GGACCCGGGA GGGCCTGGAG AGCCTGCAGG 700
 GAGGTGTGTG CCTAACCAGA GGCATGAAGG TGCTTCTCCG AGTGGGACAA 750
 AGTCCCCGAG GAGGGGCTGT CCCCCGAAAA CCTGTGTCTG AAATGCCCAT 800
 GGAAAGAGAC CGAGGGGCAG CCCACAGCCT GGAGCCTGGG AAGGAGAACC 850
 TGCCAGGTGA CCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC 900
 CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGGC 950
 GCTGCTCTTG CTGGGCGTGG CAGGGGCTGG GGGTGCCATG TGTTGGCGGA 1000
 GACGGCGGGC CAAGCCTTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC 1050
 GGGAGGGGAG GGTCTCTGGG CCTGGGGGGT GGAGGTGGGA TGGGACCTCG 1100
 GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCGGGGT GGCGGGGCTG 1150
 CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTGAGTGG TGAATATGGG 1200
 CATCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTCCAAACAT 1250
 CTACTACAAG GTATGAGGGC TCCTCTCACG TGGCTATCCT GAATCCAGCC 1300
 CTTCTTGGGG TGCTCCTCCA GTTTAATTCC TGGTTTGAGG GACACCTCTA 1350
 ACATCTCGGC CCCCTGTGCC CCCCCAGCCC CTTCACTCCT CCCGGCTGCT 1400
 GTCCTCGTCT CCACTTTTAG GATTCCTTAG GATTCCCACT GCCCACTTC 1450
 CTGCCCTCCC GTTTGGCCAT GGGTGCCCCC CTCTGTCTCA GTGTCCCTGG 1500

ATCCTTTTTC CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG 1550
 ACCCAGGCAT CCTTGTCCCC CTCACCCACC CAGAGCTAGG GGCGGGAACA 1600
 GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGCCTCTCA CTGGTTTTCT 1650
 CTTCTCTATC TCTTATTCTT TCCCTCTCTT CCGTCTCTAG GTCTGTTCTT 1700
 CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC TTGGCTTCTT 1750
 ATCCTGTGCC TCTCCCATCT CCTGGGTGGG GGCATCAAAG CATTCTCTCC 1800
 CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCTCAG 1850
 TCTGCCAAAA ATGGGGGCCT TATGGGGAAG GCTCTGACAC TCCACCCAG 1900
 CTCAGGCCAT GGGCAGCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT 1950
 ACATACTTAC TCCAGCCATT TGGGGTGGTT GGGTCATGAC AGCTACCATG 2000
 AGAAGAAGTG TCCCGTTTTG TCCAGTGGCC AATAGCAAGA TATGAACCGG 2050
 TCGGGACATG TATGGACTTG GTCTGATGCT GAATGGGCCA CTTGGGACCG 2100
 GAAGTGAAGT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGCC 2150
 TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTTATCCAG 2200
 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAAGTCCAA 2250
 GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT 2300
 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAAGTT 2350
 ACTGACTGTA AGAGGTTAGA GGTGGACCGA 2380

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Pro	Pro	His	Ser	Gly	Pro	Gly	Gly	Val	Arg	Val	Gly	Ala
1				5				10					15	
Leu	Leu	Leu	Leu	Gly	Val	Leu	Gly	Leu	Val	Ser	Gly	Leu	Ser	Leu
				20				25					30	

Glu	Pro	Val	Tyr	Trp	Asn	Ser	Ala	Asn	Lys	Arg	Phe	Gln	Ala	Glu	35	40	45
Gly	Gly	Tyr	Val	Leu	Tyr	Pro	Gln	Ile	Gly	Asp	Arg	Leu	Asp	Leu	50	55	60
Leu	Cys	Pro	Arg	Ala	Arg	Pro	Pro	Gly	Pro	His	Ser	Ser	Pro	Asn	65	70	75
Tyr	Glu	Phe	Tyr	Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	80	85	90
Arg	Cys	Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	95	100	105
Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	110	115	120
Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	125	130	135
Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	140	145	150
Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	155	160	165
Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	170	175	180
Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	185	190	195
Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	200	205	210
Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	215	220	225
Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	230	235	240
Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	245	250	255
Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	260	265	270
Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	275	280	285

Arg Glu Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly
290 295 300

Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys Val Ser
305 310 315

Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln Asp Gly Pro Pro
320 325 330

Gln Ser Pro Pro Asn Ile Tyr Tyr Lys Val
335 340

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCCGACGCTG TGAGGCACCC CCTGCCCCAA ACCTCCTTCT CACTTGTGAT 50
CGCCCAGACC TGGATCTCCG CTTACCATC AAGTTCCAGG AGTATAGCCC 100
TAATCTCTGG GGCCACGAGT TCCGCTCGCA CCACGATTAC TACATCATTG 150
CCACATCGGA TGGGACCCGG GAGGCCTGGG AGAGCCTGCA GGGAAGTGTG 200
TGCCTAACCA GAGGCATGAA GGTGCTTCTC CGAGTNGGAC AAAGTCCCGA 250
GGAGGGGCTG TCCCCGAAA ACCTGTGTCT GAAATGCCCA TGGAAGAGA 300
CCGAGGGGCA GCCCACAGCC TGGGAGCCTG GGGAAGGAGA ACCTGCCAGG 350
TGACCCACC AGCAATNCAA CCTTCCGGGG TTGCTTGAAG GGCCCCTTGA 400
CCCTTTCCCA GCATTGCNTG CANTTGTTN GGGGCAGCAN GGGGNGTTT 450
TGGC 454

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACAAAGTC CCGAGGAGGG GCTGTCCCCC GAAAACCTGT GTCTGAAATG 50
CCCATGGAAA 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTTCTCC TTCCCCAGGC TCCCAGGCTG TGGGCTGCCC CTCGGTCTCT 50
TTCCATGGGC 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Pro Gly Gln Arg Trp Leu Gly Lys Trp Leu Val Ala
1 5 10 15
Met Val Val Trp Ala Leu Cys Arg Leu Ala Thr Pro Leu Ala Lys
20 25 30

Asn	Leu	Glu	Pro	Val	Ser	Trp	Ser	Ser	Leu	Asn	Pro	Lys	Phe	Leu	35	40	45
Ser	Gly	Lys	Gly	Leu	Val	Ile	Tyr	Pro	Lys	Ile	Gly	Asp	Lys	Leu	50	55	60
Asp	Ile	Ile	Cys	Pro	Arg	Ala	Glu	Ala	Gly	Arg	Pro	Tyr	Glu	Tyr	65	70	75
Tyr	Lys	Leu	Tyr	Leu	Val	Arg	Pro	Glu	Gln	Ala	Ala	Ala	Cys	Ser	80	85	90
Thr	Val	Leu	Asp	Pro	Asn	Val	Leu	Val	Thr	Cys	Asn	Arg	Pro	Glu	95	100	105
Gln	Glu	Ile	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Phe	Ser	Pro	Asn	110	115	120
Tyr	Met	Gly	Leu	Glu	Phe	Lys	Lys	His	His	Asp	Tyr	Tyr	Ile	Thr	125	130	135
Ser	Thr	Ser	Asn	Gly	Ser	Leu	Glu	Gly	Leu	Glu	Asn	Arg	Glu	Gly	140	145	150
Gly	Val	Cys	Arg	Thr	Arg	Thr	Met	Lys	Ile	Ile	Met	Lys	Val	Gly	155	160	165
Gln	Asp	Pro	Asn	Ala	Val	Thr	Pro	Glu	Gln	Leu	Thr	Thr	Ser	Arg	170	175	180
Pro	Ser	Lys	Glu	Ala	Asp	Asn	Thr	Val	Lys	Met	Ala	Thr	Gln	Ala	185	190	195
Pro	Gly	Ser	Arg	Gly	Ser	Leu	Gly	Asp	Ser	Asp	Gly	Lys	His	Glu	200	205	210
Thr	Val	Asn	Gln	Glu	Glu	Lys	Ser	Gly	Pro	Gly	Ala	Ser	Gly	Gly	215	220	225
Ser	Ser	Gly	Asp	Pro	Asp	Gly	Phe	Phe	Asn	Ser	Lys	Val	Ala	Leu	230	235	240
Phe	Ala	Ala	Val	Gly	Ala	Gly	Cys	Val	Ile	Phe	Leu	Leu	Ile	Ile	245	250	255
Ile	Phe	Leu	Thr	Val	Leu	Leu	Leu	Lys	Leu	Arg	Lys	Arg	His	Arg	260	265	270
Lys	His	Thr	Gln	Gln	Arg	Ala	Ala	Ala	Leu	Ser	Leu	Ser	Thr	Leu	275	280	285

Ala	Ser	Pro	Lys	Gly	Gly	Ser	Gly	Thr	Ala	Gly	Thr	Glu	Pro	Ser
				290					295					300
Asp	Ile	Ile	Ile	Pro	Leu	Arg	Thr	Thr	Glu	Asn	Asn	Tyr	Cys	Pro
				305					310					315
His	Tyr	Glu	Lys	Val	Ser	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile
				320					325					330
Val	Gln	Glu	Met	Pro	Pro	Gln	Ser	Pro	Ala	Asn	Ile	Tyr	Tyr	Lys
				335					340					345
Val														
346														

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Val	Arg	Arg	Asp	Ser	Val	Trp	Lys	Tyr	Cys	Trp	Gly	Val
1				5					10					15
Leu	Met	Val	Leu	Cys	Arg	Thr	Ala	Ile	Ser	Lys	Ser	Ile	Val	Leu
				20					25					30
Glu	Pro	Ile	Tyr	Trp	Asn	Ser	Ser	Asn	Ser	Lys	Phe	Leu	Pro	Gly
				35					40					45
Gln	Gly	Leu	Val	Leu	Tyr	Pro	Gln	Ile	Gly	Asp	Lys	Leu	Asp	Ile
				50					55					60
Ile	Cys	Pro	Lys	Val	Asp	Ser	Lys	Thr	Val	Gly	Gln	Tyr	Glu	Tyr
				65					70					75
Tyr	Lys	Val	Tyr	Met	Val	Asp	Lys	Asp	Gln	Ala	Asp	Arg	Cys	Thr
				80					85					90
Ile	Lys	Lys	Glu	Asn	Thr	Pro	Leu	Leu	Asn	Cys	Ala	Lys	Pro	Asp
				95					100					105
Gln	Asp	Ile	Lys	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Phe	Ser	Pro	Asn
				110					115					120
Leu	Trp	Gly	Leu	Glu	Phe	Gln	Lys	Asn	Lys	Asp	Tyr	Tyr	Ile	Ile
				125					130					135

Ser	Thr	Ser	Asn	Gly	Ser	Leu	Glu	Gly	Leu	Asp	Asn	Gln	Glu	Gly	
				140					145					150	
Gly	Val	Cys	Gln	Thr	Arg	Ala	Met	Lys	Ile	Leu	Met	Lys	Val	Gly	
				155					160					165	
Gln	Asp	Ala	Ser	Ser	Ala	Gly	Ser	Thr	Arg	Asn	Lys	Asp	Pro	Thr	
				170					175					180	
Arg	Arg	Pro	Glu	Leu	Glu	Ala	Gly	Thr	Asn	Gly	Arg	Ser	Ser	Thr	
				185					190					195	
Thr	Ser	Pro	Phe	Val	Lys	Pro	Asn	Pro	Gly	Ser	Ser	Thr	Asp	Gly	
				200					205					210	
Asn	Ser	Ala	Gly	His	Ser	Gly	Asn	Asn	Ile	Leu	Gly	Ser	Glu	Val	
				215					220					225	
Ala	Leu	Phe	Ala	Gly	Ile	Ala	Ser	Gly	Cys	Ile	Ile	Phe	Ile	Val	
				230					235					240	
Ile	Ile	Ile	Thr	Leu	Val	Val	Leu	Leu	Leu	Lys	Tyr	Arg	Arg	Arg	
				245					250					255	
His	Arg	Lys	His	Ser	Pro	Gln	His	Thr	Thr	Thr	Leu	Ser	Leu	Ser	
				260					265					270	
Thr	Leu	Ala	Thr	Pro	Lys	Arg	Ser	Gly	Asn	Asn	Asn	Gly	Ser	Glu	
				275					280					285	
Pro	Ser	Asp	Ile	Ile	Ile	Pro	Leu	Arg	Thr	Ala	Asp	Ser	Val	Phe	
				290					295					300	
Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	Gly	Asp	Tyr	Gly	His	Pro	Val	
				305					310					315	
Tyr	Ile	Val	Gln	Glu	Met	Pro	Pro	Gln	Ser	Pro	Ala	Asn	Ile	Tyr	
				320					325					330	
Tyr	Lys	Val													
				333											